

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH MUS MUSCULUS INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN SEQ IN NO:13

Query: IGFBP\_like protein (SEQ ID NO: 6)

Subject: >gi|9055246 (AB006141) IGFBP-like protein [Mus musculus] SEQ ID NO: 13

Length = 270

Score = 1170 (416.9 bits), Expect = 1.8e-118, P = 1.8e-118

Identities = 209/269 (77%), Positives = 232/269 (86%)

Query: 8 LPLLLLLLLLPPLSPSLGIRDVGRRPKGCRPEGCPAPAPCPAPGISALDECGCCA 67

+P L LLLL LLP L+ LG+RD G R P+C PC+ + CPAP+PCPAP ISA DECGCCA

1 MPRLPLLLL-LLPSLARGGLRDAGRHRHECSPCQQDRCAPSPCAPWISARDECGCCA 59

Query: 68 RCLGAEGASCGRAGRCGPGLVCASQAAGAAPEGTGLCVCAQRGTVCGSDGRSYPVCA 127

RCLGAEGASCGG G RCGPGLVCAS+A+G APEGTGLCVCAQRG VCGSDGRSY S+CA

Sbjct: 60 RCLGAEGASCGGPGVSRGCGPLVCASRASGTAPEGTGLCVCAQRGAVCGSDGRSYSSICA 119

Query: 128 LRLRARHTPRAHPGHLHKARDGPCFAPVVVPPRSVHNVTGAQVGLSCEVRAVPTPVIT 187

LRLRAH PRAH GHLHKARDGCFEAPV++PPR +HNVTG QV LSCEV+AVTTPVIT

Sbjct: 120 LRLRARHAPRAHHGLHKARDGCPCEFAPVVLMPPRDIHNVTGTQVFLSCEVKA VPTPVIT 179

Query: 188 WRKVTKSPEGTQALEELPGDHVNIAVQVRGGPSDHEATAWILINPLRKEDEGVYQCHAAN 247

W+KV SPECT+ LEELPGDHVNIAVQVRGGPSDHE T+WILINPLRKEDEGVY CHAAN

Sbjct: 180 WKKVKHSPGTEGLEELPGDHVNIAVQVRGGPSDHETTSWILINPLRKEDEGVYHCHAAAN 239

Query: 248 MVGEAESHSTVTVLDLSKYRSFHFAPDD 276

+GEA+SH TVTVL<sub>DL</sub>+Y+S + P D

Subjct: 240 AIGEAQSHGTVTVLDLNRKSLYSSVPGD 268

**FIG. 1**

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH HOMO SAPIENS PROSTOGLANDIN I2 SEQ NO:14

Query: IGFBP\_like protein (SEQ ID NO: 6)  
 Subject: >gi|1082724 Prostaglandin I2 [Homo sapiens (SEQ ID NO: 14)]  
 Length: 273

Score = 570 (205.7 bits), Expect = 7.9e-61, P = 7.9e-61  
 Identities = 123/273 (45%), Positives = 150/273 (54%)

Query:	4	PSLRALLGAAGLLLLLL--PLSSSS--SDT-----CGPCEPASCPLPLGCLLGETR	54
		P L +LLL LLLL L PLS S D CGPC P CP P	
Sbjct:	2	PRL-SLLPLLLLLLLLLPLPLSPSLGIRDVGRRPKCGPCRPEGCPAPAPCAPGISAL	60
Query:	55	DACGCCPMARGEPEPCGGGAGRGYCAPMECVKSRKRRKGAGAAAGPGVSGVCVK	114
		D CGCC C EG CGG GR C PG+ C AGAA G +G+CVC	
Sbjct:	61	DECGCCARCLGAEGASCGRAGGR--CGPGLVCASQA-----AGAAPEG--TGLCVCA	109
Query:	115	SRYPVCGSDGTTYPSCQLRAASQRAESRGEKAITQVSKGTCEQGPSIVTPPKDIWNVTG	174
		R VCGSDG +YPS C LR ++ + + G CE P +V PP+ + NVTG	
Sbjct:	110	QRGTVCGSDGRSYPSPVCALRLRARHTPRAHPGHLHKARDGPCEFAFPVVVPPRSVHNVTG	169
Query:	175	AQVYLSCEVIGIPTPVLINWKVRGHYGVQRTPELLPGDRDNLAIQTRGGPEKHEVTGWVL	234
		AQV LSCEV +PTPV+ W KV + G Q E LPGD N+A+Q RGGP HE T W+L	
Sbjct:	170	AQVGLSCEVRAVPTPVITWRKVTKSPEGTQALEELPGDHVNIQVVRGGPSDHEATAWIL	229
Query:	235	VSPLSKEDAGEYECHASNSQQAASAKITVVD	267
		++PL KED G Y+CHA+N G+A + + +TV+D	
Sbjct:	230	INPLRKEDEGVYQCHAANMVGEAESHSTVTVLD	262

FIG. 2